```
    GAATTCGGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCC
  1 ---------+---------+---------+---------+---------+---------+ 60

    ATCCGAAAGAGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAAC
 61 ---------+---------+---------+---------+---------+---------+ 120

    AGTCAGAGACCCTCCTGAAAGCAGGAGACGGACGGTACCCCTCCGGCTCTGCGGGGCGG
121 ---------+---------+---------+---------+---------+---------+ 180

    CTGCGGCCCCTCCGTTCTTTCCCCCTCCCCGAGAGACACTCTTCCTTTCCCCCCACGAAG
181 ---------+---------+---------+---------+---------+---------+ 240

    ACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCCATGGAGGCCGCTTCCTGCTGACG
241 ---------+---------+---------+---------+---------+---------+ 300
```

FIG. 1A

```
    CTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGCTCCGGGGTGTTCGAG
301 ---------+---------+---------+---------+---------+---------+ 360

    CTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGCTGCCGG
361 ---------+---------+---------+---------+---------+---------+ 420

    GGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTC
421 ---------+---------+---------+---------+---------+---------+ 480

    TGCCTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCC
481 ---------+---------+---------+---------+---------+---------+ 540

    ATCACCCCCGTCCTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGAC
541 ---------+---------+---------+---------+---------+---------+ 600

    CCCGCCTTCAGCAACCCCATCCGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCG
601 ---------+---------+---------+---------+---------+---------+ 660

    CTCATCATCGAGGCTCTGCACACCGACTCCCCCGACGACCTCACCACAGAAAACCCCGAG
661 ---------+---------+---------+---------+---------+---------+ 720
```

FIG. 1A (cont'd)

```
     CGCCTCATCAGCCGCCTGGCCACCCAGAGGCACCTGGCGGTGGGCGAGGAGTGGTCCCAG
 721 ---------+---------+---------+---------+---------+---------+ 780

     GACCTGCACAGCAGCGGCCGGACCGACCTCAAGTACTCCTATCGCTTTGTGTGTGATGAG
 781 ---------+---------+---------+---------+---------+---------+ 840

     CACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGTCAC
 841 ---------+---------+---------+---------+---------+---------+ 900

     TTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGC
 901 ---------+---------+---------+---------+---------+---------+ 960

     ACTGAGCCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGG
 961 ---------+---------+---------+---------+---------+---------+ 1020

     GAATGCAAGTGCAGAGTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCA
1021 ---------+---------+---------+---------+---------+---------+ 1080

     GGCTGCCTGCACGGTACCTGTCAGCAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGC
1081 ---------+---------+---------+---------+---------+---------+ 1140
```

FIG. 1A (cont'd)

```
     GGCCTTTTCTGCAACCAGGACCTGAACTACTGCACTCACCACAAGCCATGCAAGAATGGT
1141 ---------+---------+---------+---------+---------+---------+ 1200

1201 ---------+---------+---------+---------+---------+---------+ 1260
     CGGTGTACGTGGTTGTGGCCAGTCCCCTCCATGTGAACAAGAACGGCTGGACCCATGTGT

     GGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAGAATGGTGGA
1261 ---------+---------+---------+---------+---------+---------+ 1320

     AGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380

     AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGC
1381 ---------+---------+---------+---------+---------+---------+ 1440

     ACTGACAACCCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAAC
1441 ---------+---------+---------+---------+---------+---------+ 1500

     TGTGAAAAGAAAATCGATTACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTT
1501 ---------+---------+---------+---------+---------+---------+ 1560
```

FIG. 1A (cont'd)

```
     GACCTGGGGAACTCCTACATATGCCAGTGCCAGGCTGGCTTCACTGGCAGGCACTGTGAC
1561 ---------+---------+---------+---------+---------+---------+ 1620

     GACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTCAATGGAGGGACCTGTCAGGATGGG
1621 ---------+---------+---------+---------+---------+---------+ 1680

     GTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAGAACTGCAGCACGCCG
1681 ---------+---------+---------+---------+---------+---------+ 1740

     GTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGAAGCAAC
1741 ---------+---------+---------+---------+---------+---------+ 1800

     CGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCC
1801 ---------+---------+---------+---------+---------+---------+ 1860

     GAGCCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAAC
1861 ---------+---------+---------+---------+---------+---------+ 1920

     AGCCAGTTTCCCTGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTG
1921 ---------+---------+---------+---------+---------+---------+ 1980
```

FIG. 1A (cont'd)

```
      TACCAGTCGGTGTACGTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTG
2401  ---------+---------+---------+---------+---------+---------+  2460

      TAAAACAGACGTGACGTGGCAAAGCTTATCGATACCGTCATCAAGCTT
2461  ---------+---------+---------+---------+--------  2508
```

FIG. 1A (cont'd)

1 GAATTCGGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCCATCCGAAAG 69

70 AGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAACAGTCAGAGACCCTCCTGA 138

139 AAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGGCTGCGGCCCCTCCGTTCTTTCCCCCTC 207

208 CCCGAGAGACACTCTTCCTTTCCCCCCACGAAGACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCC 276

277 ATGGGAGGCCGCTTCCTGCTGACGCTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGC 345

346 TCCGGGGTGTTCGAGCTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGC 414

415 TGCCGGGGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTCTGC 483

FIG. 1B

484 CTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCCA

553 CTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGACCCCGCCTTCA

622 CGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCGCTCATCATCGAGGCTCTGC

691 CCCGACGACCTCACCACAGAAAACCCCGAGCGCCTCATCAGCCGCCTGGCCACCCAGA

760 GTGGGCGAGGAGTGGTCCCAGGACCTGCACAGCAGCGGCCGCACCCGACCTCAAGTAC

FIG. 1B (cont'd)

GTGTGATGAGCACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGT 897

898 CACTTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGCACTGAG 966

967 CCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGGGAATGCAAGTGCAGA 1035

1036 GTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCAGGCTGCCTGCACGGTACCTGTCAG 1104

1105 CAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGCGGCCTTTTCTGCAACCAGGACCTGAACTACTGC 1173

1174 ACTCACCACAAGCCATGCAAGAATGGTGCCACATGCACCAACACCGGTCAGGGGAGCTACACTTGTTCT 1242

1243 TGCCGACCTGGGTACACAGGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAG 1311

FIG. 1B (cont'd)

1312 AATGGTGGAAGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA 1380

1381 AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGCACTGACAAC 1449

1450 CCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAACTGTGAAAAGAAAATCGAT 1518

1519 TACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTTGACCTGGGGAACTCCTACATATGCCAG 1587

1588 TGCCAGGCTGGCTTCACTGGCAGGCACTGTGACGACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTC 1656

1657 AATGGAGGGACCTGTCAGGATGGGGTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAG 1725

FIG. 1B (cont'd)

1726 AACTGCAGCACGCCGGTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGA 1794

1795 AGCAACCGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCCGAG 1863

1864 CCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAACAGCCAGTTTCCC 1932

1933 TGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTGGGTTGCGCCGCCATCGTCGTC 2001

2002 TGCGTCAGGCTGAAGGTGCAGAAGAGGCACCACCAGCCGGAGGCCTGCAGGAGTGAAACGGAGACCATG 2070

2071 AACAACCTGGCGAACTGCCAGCGCGAGAAGGACATCTCCATCAGCGTCATCGGTGCCACTCAGATTAAA 2139

2140 AACACAAATAAGAAAGTAGACTTTCACAGCGATAACTCCGATAAAAACGGCTACAAAGTTAGATACCCA 2208

FIG. 1B (cont'd)

2209 TCAGTGGATTACAATTTGGTGCATGAACTCAAGAATGAGGACTCTGTGAAAGAGGAGCATGGCAAATGC 2277

2278 GAAGCCAAGTGTGAAACGTATGATTCAGAGGCAGAAGAGAAAAGCGCAGTACAGCTAAAAAGTAGTGAC 2346

2347 ACTTCTGAAAGAAAACGGCCAGATTCAGTATATTCCACTTCAAAGGACACAAAGTACCAGTCGGTGTAC 2415

2416 GTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTTAGTATCCCACCTGGCAGTCGGACA 2484

2485 AGTCTTGGTGTGTGATTCCCATCCAGCGCAGGTCAGGGCGGCCAAACCATTCTACCTGCTGCCACAGTC 2553

2554 ATCTGTACCCAATGAAAACTGGCCACCTTCAGTCTGTGGCACTGCAGACGTTGAAAAAACTTGTTGTGG 2622

FIG. 1B (cont'd)

2623 ATTAACATAAGCTCCAGTGGGGGTTACAGGGACAGCAATTTTTGCAGGCAAGGGTATAACTGTAGTGCA 2691

2692 GTTGTAGCTTACTAACCCTACTGACTCATTCTTTCGTGTGCTTCCTGCAGAGCCTGTTTTTGCTTGGCA 2760

2761 TTGAGGTGAAGTCCTGACCCTCTGCATCCTCATAGTCCTCTGCTTTCTTTTTATTAACCTCTTCTGGTC 2829

2830 TCTGCTTGTGTTTTCTCTCAACAGGTGTAAAACAGACGTGACGTGGCAAAGCTT 2883

FIG. 1B (cont'd)

```
  1 MGGRFLLTLA LLSALLCRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG GPGGAGQQQC
 61 DCKTFFRVCL KHYQASVSPE PPCTYGSAIT PVLGANSFSV PDGAGGADPA FSNPIRFPFG
121 FTWPGTFSLI IEALHTDSPD DLTTENPERL ISRLATQRHL AVGEEWSQDL HSSGRTDLKY
181 SYRFVCDEHY YGEGCSVFCR PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPGCDEQ
241 HGFCDKPGEC KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT
301 HHKPCKNGAT CTNTGQGSYT CSCRPGYTGS SCEIEINECD ANPCKNGGSC TDLENSYSCT
361 CPPGFYGKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC PLGYSGFNCE KKIDYCSSSP
421 CANGAQCVDL GNSYICQCQA GFTGRHCDDN VDDCASFPCV NGGTCQDGVN DYSCTCPPGY
481 NGKNCSTPVS RCEHNPCHNG ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT
541 EKYTEGQNSQ FPWIAVCAGI ILVLMLLLGC AAIVVCVRLK VQKRHHQPEA CRSETETMNN
601 LANCQREKDI SISVIGATQI KNTNKKVDFH SDNSDKNGYK VRYPSVDYNL VHELKNEDSV
661 KEEHGKCEAK CETYDSEAEE KSAVQLKSSD TSERKRPDSV YSTSKDTKYQ SVYVISEEKD
721 ECIIATEV
```

FIG. 2

```
C-Delta-1    1  MGGRFLLTLA-LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC   60
X-Delta-1    1  MGQQRMLTLL-VLSAVL--CQISCSGLFELRLQEFVNKKGLLGNMNCCRPGSL--ASLQRC   56
Delta        1  --MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLG   59

C-Delta-1   61  DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGF  121
X-Delta-1   57  ECKTFFRICLKHYQSNVSPEPPCTYGGAVTPVLGTNSFVVPES-SNADPTFSNPIRFPFGF  116
Delta       60  SCKTRFRLCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSF  120

C-Delta-1  122  TWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSY  182
X-Delta-1  117  TWPGTFSLIIEAIHADSADDLNTENPERLISRLATQRHLTVGEQWSQDLHSSDRTELKYSY  177
Delta      121  SWPGTFSLIVEAWH-DTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDF  180

C-Delta-1  183  RFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGF  243
X-Delta-1  178  RFVCDEYYYGEGCSDYCRPRDDAFGHFSCGERGEKLCNPGWKGLYCTEPICLPGCDEHHGY  238
Delta      181  RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE--HGH  239
                                     DSL

C-Delta-1  244  CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP  304
X-Delta-1  239  CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP  299
Delta      240  CDKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRP  300
                EGF1                         EGF2

C-Delta-1  305  CKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDA--NPCKNGGSCTD---LENSYSCT  360
X-Delta-1  300  CENGATCTNTGQGSYTCSCRPGYTGSNCEIEVNECDA--NPCKNGGSCSD---LENSYTCS  355
Delta      301  CKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCH  361
                      EGF3                                   EGF4

C-Delta-1  361  CPPGFYGKNCELSAMTCADGPCFNG-----GRCTDNPDGGYSCRCPLGYSGFNCEKKIDYC  416
X-Delta-1  356  CPPGFYGKNCELSAMTCADGPCFNG-----GRCADNPDGGYICFCPGVYSGFNCEKKIDYC  411
Delta      362  CRNGWSGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNC  422
                                           EGF5

C-Delta-1  417  SSSPCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCP  477
X-Delta-1  412  SSNPCANGARCEDLGNSYICQCQEGFSGRNCDDNLDDCTSFPCQNGGTCQDGINDYSCTCP  472
Delta      423  SPNPCINGGSCQPSGK---CICPSGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCV  480
                      EGF6                                  EGF7

C-Delta-1  478  PGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGP----  534
X-Delta-1  473  PGYIGKNCSMPITKCEHNPCHNGATCHERNNRYVCQCARGYGGNNCQFLLPE---------  524
Delta      481  PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHNG  541
                                   EGF8

C-Delta-1  535  ---------------------------VIVDFTE--KYTEGQNSQFPW--IAVCAGIILVL  564
X-Delta-1  525  ------------------------EKPVVVDLTE--KYTEGQSGQFPW--IAVCAGIVLVL  557
Delta      542  GTCMNRVNSPECVCANGFRGKQCDEESYDSVTFDAHQYGATTQARADGLANAQVVLIAVFS  602
                   EGF9

C-Delta-1  565  MLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCQREKD--ISISVIGATQIKNT  623
X-Delta-1  558  MLLLGCAAVVVCVRVRVQKRRHQPEACRGESKTMNNLANCQREKD--ISVSFIGTTQIKNT  616
Delta      603  VAMPLVAVIAACVVFCMKRKRKRAQEKDNAEARKQNEQNAVATMHHNGSAVGVALASASMG  663
                 TM

C-Delta-1  624  NKKVDFHSD-NSDKNGYKVRYPSVDYNLVHELKNEDSVKEEHGKCEAKCETYDSEAEEKSA  683
X-Delta-1  617  NKKIDFLSESNNEKNGYKPRYPSVDYNLVHELKNEDSPKEERSKCEAKCSSNDSDSEDVNS  677
Delta      664  GKTGSNSGLTFDGGNPNIIKNTWDKSVN-NICASAAAAAAAAAAADECLMYGGYVASVADN  723

C-Delta-1  684  -----VQLKSSDTSERK---------RPDSVYSTSKDTKYQSVYVISEEKDECIIATEV   728
X-Delta-1  678  -----VHSK-RDSSERR---------RPDSAYSTSKDTKYQSVYVISDEKDECIIATEV   721
Delta      724  NNANSDFCVAPLQRAKSQKQLNTDPTLMHRGSPAGTSAKGASGGGPGAAEGKRISVLGEGS  784

Delta      785  YCSQRWPSLAAAGVAGACSSQLMAAASAAGTDGTAQQQRSVVCGTPHM               832
```

FIG. 3

```
C-Delta-1     184  V-CDEHYYGE G-CSVFCRPR DDRFGHFTCG ERGEKVCNPG WKGQYC  228
Delta         182  VTCDLNYYGS G-CAKFCRPR DDSFGHSTCS ETGEIICLTG WQGDYC  226
Serrate       235  VQCAVTYYNT TFCTTFCRPR DDQFGHYACG SEGQKLCLNG WQGVNC  279
C-Serrate-1        VTCAEHYYGF G-CNKFCRPR DDFFTHHTCD QNGNKTCLEG WTGPEC

apx-1         130  NLCSSNYHGK R-CNRYCIAN -AKLHWE-CS THGVRRCSAG WSGEDC  172
lag-2         120  VTCARNYFGN R-CENFCDAH LAKAARKRCD AMGRLRCDIG WMGPHC  166
```

FIG. 4

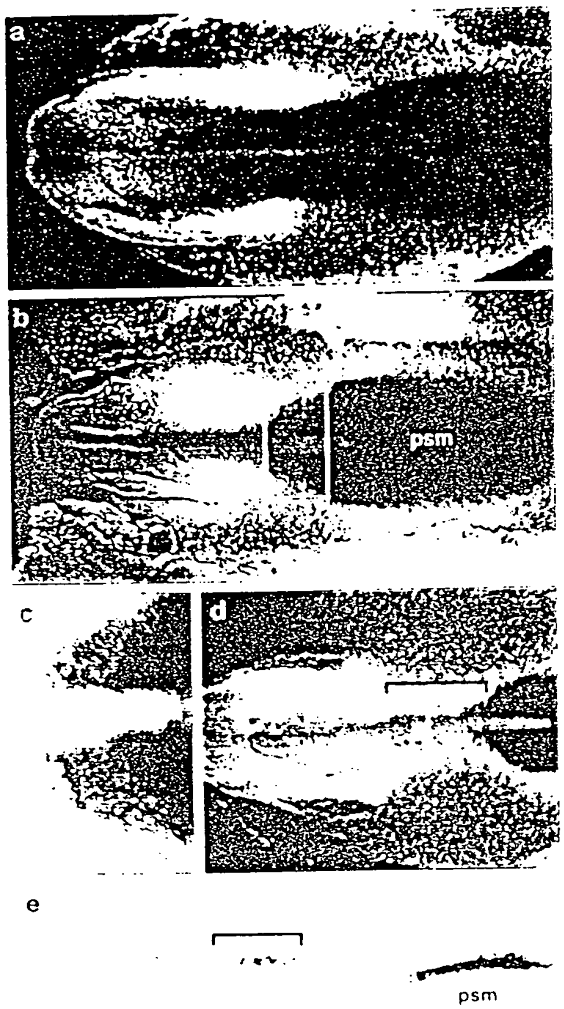

FIG. 5

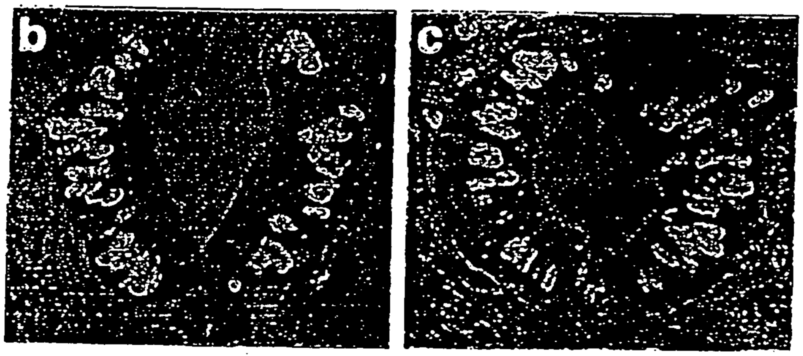

FIG. 6B FIG. 6C

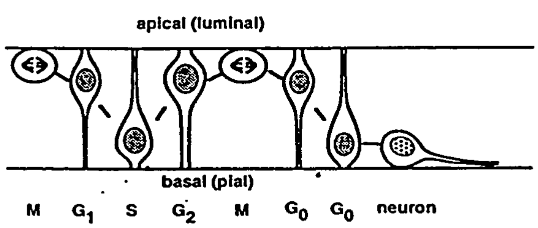

FIG. 6A

```
CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCCATGGGCC GTCGGAGCGC GCTAGCCCTT   60
GCCGTGGTCT CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  120
CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG CGGGGGCTCT  180
GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC TCAAGCACTA CCAGGCCAGC  240
GTGTCACCGG AGCCACCCTG CACCTACGGC AGTGCCGTCA CGCCAGTGCT GGGTGTCGAC  300
TCCTTCAGCC TGCCTGATGG CGCAGGCATC GACCCCGCCT TCAGCAACCC CATCCGATTC  360
CCCTTCGGCT TCACCTGGCC AGGTACCTTC TCTCTGATCA TTGAAGCCCT CCATACAGAC  420
TCTCCCGATG ACCTCGCAAC AGAAAACCCA GAAAGACTCA TCAGCCGCCT GACCACACAG  480
AGGCACCTCA CTGTGGGAGA AGAATGGTCT CAGGACCTTC ACAGTAGCGG CCGCACAGAC  540
CTCCGGTACT CTTACCGGTT TGTGTGTGAC GAGCACTACT ACGGAGAAGG TTGCTCTGTG  600
TTCTGCCGAC CTCGGGATGA CGCCTTTGGC CACTTCACCT GCGGGGACAG AGGGGAGAAG  660
ATGTGCGACC CTGGCTGGAA AGGCCAGTAC TGCACTGACC CAATCTGTCT GCCAGGGTGT  720
GATGACCAAC ATGGATACTG TGACAAACCA GGGGAGTGCA AGTGCAGAGT TGGCTGGCAG  780
GGCCGCTACT GCGATGAGTG CATCCGATAC CCAGGTTGTC TCCATGGCAC CTGCCAGCAA  840
CCCTGGCAGT GTAACTGCCA GGAAGGCTGG GGGGGCCTTT TCTGCAACCA AGACCTGAAC  900
TACTGTACTC ACCATAAGCC GTGCAGGAAT GGAGCCACCT GCACCAACAC GGGCCAGGGG  960
AGCTACACAT GTTCCTGCCG ACCTGGGTAT ACAGGTGCCA ACTGTGAGCT GGAAGTAGAT 1020
GAGTGTGCTC CTAGCCCCTG CAAGAACGGA GCGAGCTGCA CGGACCTTGA GGACAGCTTC 1080
TCTTGCACCT GCCCTCCCGG CTTCTATGGC AAGGTCTGTG AGCTGAGCGC CATGACCTGT 1140
GCAGATGGCC CTTGCTTCAA TGGAGGACGA TGTTCAGATA ACCCTGACGG AGGCTACACC 1200
TGCCATTGCC CCTTGGGCTT CTCTGGCTTC AACTGTGAGA AGAAGATGGA TCTCTGCGGC 1260
TCTTCCCCTT GTTCTAACGG TGCCAAGTGT GTGGACCTCG GCAACTCTTA CCTGTGCCGG 1320
TGCCAGGCTG GCTTCTCCGG GAGGTACTGC GAGGACAATG TGGATGACTG TGCCTCCTCC 1380
CCGTGTGCAA ATGGGGGCAC CTGCCGGGAC AGTGTGAACG ACTTCTCCTG TACCTGCCCA 1440
CCTGGCTACA CGGGCAAGAA CTGCAGCGCC CCTGTCAGCA GGTGTGAGCA TGCACCCTGC 1500
CATAATGGGG CCACCTGCCA CCAGAGGGGC CAGCGCTACA TGTGTGAGTG CGCCCAGGGC 1560
TATGGCGGCC CCAACTGCCA GTTTCTGCTC CCTGAGCCAC CACCAGGGCC CATGGTGGTG 1620
GACCTCAGTG AGAGGCATAT GGAGAGCCAG GGCGGGCCCT TCCCCTGGGT GGCCGTGTGT 1680
GCCGGGGTGG TGCTTGTCCT CCTGCTGCTG CTGGGCTGTG CTGCTGTGGT GGTCTGCGTC 1740
CGGCTGAAGC TACAGAAACA CCAGCCTCCA CCTGAACCCT GTGGGGGAGA GACAGAAACC 1800
ATGAACAACC TAGCCAATTG CCAGCGCGAG AAGGACGTTT CTGTTAGCAT CATTGGGGCT 1860
ACCCAGATCA AGAACACCAA CAAGAAGGCG GACTTTCACG GGGACCATGG AGCCGAGAAG 1920
AGCAGCTTTA AGGTCCGATA CCCCACTGTG GACTATAACC TCGTTCGAGA CCTCAAGGGA 1980
GATGAAGCCA CGGTCAGGGA TACACACAGC AAACGTGACA CCAAGTGCCA GTCACAGAGC 2040
TCTGCAGGAG AAGAGAAGAT CGCCCCAACA CTTAGGGGTG GGGAGATTCC TGACAGAAAA 2100
AGGCCAGAGT CTGTCTACTC TACTTCAAAG GACACCAAGT ACCAGTCGGT GTATGTTCTG 2160
TCTGCAGAAA AGGATGAGTG TGTTATAGCG ACTGAGGTGT AAGATGGAAG CGATGTGGCA 2220
AAATTCCCAT TTCTCTTAAA TAAAATTCCA AGGATATAGC CCCGATGAAT GCTGCTGAGA 2280
GAGGAAGGGA GAGGAAACCC AGGGACTGCT GCTGAGAACC AGGTTCAGGC GAACGTGGTT 2340
CTCTCAGAGT TAGCAGAGGC GCCCGACACT GCCAGCCTAG GCTTTGGCTG CCGCTGGACT 2400
GCCTGCTGGT TGTTCCCATT GCACTATGGA CAGTTGCTTT GAAGAGTATA TATTTAAATG 2460
GACGAGTGAC TTGATTCATA TAGGAAGCAC GCACTGCCCA CACGTCTATC TTGGATTACT 2520
ATGAGCCAGT CTTTCCTTGA ACTAGAAACA CAACTGCCTT TATTGTCCTT TTTGATACTG 2580
AGATGTGTTT TTTTTTTTTC CTAGACGGGA AAAAGAAAAC GTGTGTTATT TTTTTTGGGA 2640
TTTGTAAAAA TATTTTTCAT GATTATGGGA GAGCTCCCAA CGCGTTGGAG GT         2692
```

FIG. 7

```
MGRRSALALA VVSALLCQVW SSGVFELKLQ EFVNKKGLLG NRNCCRGGSG    50
PPCACRTFFR VCLKHYQASV SPEPPCTYGS AVTPVLGVDS FSLPDGAGID   100
PAFSNPIRFP FGFTWPGTFS LIIEALHTDS PDDLATENPE RLISRLTTQR   150
HLTVGEEWSQ DLHSSGRTDL RYSYRFVCDE HYYGEGCSVF CRPRDDAFGH   200
FTCGDRGEKM CDPGWKGQYC TDPICLPGCD DQHGYCDKPG ECKCRVGWQG   250
RYCDECIRYP GCLHGTCQQP WQCNCQEGWG GLFCNQDLNY CTHHKPCRNG   300
ATCTNTGQGS YTCSCRPGYT GANCELEVDE CAPSPCKNGA SCTDLEDSFS   350
CTCPPGFYGK VCELSAMTCA DGPCFNGGRC SDNPDGGYTC HCPLGFSGFN   400
CEKKMDLCGS SPCSNGAKCV DLGNSYLCRC QAGFSGRYCE DNVDDCASSP   450
CANGGTCRDS VNDFSCTCPP GYTGKNCSAP VSRCEHAPCH NGATCHQRGQ   500
RYMCECAQGY GGPNCQFLLP EPPPGPMVVD LSERHMESQG GPFPWVAVCA   550
GVVLVLLLLL GCAAVVVCVR LKLQKHQPPP EPCGGETETM NNLANCQREK   600
DVSVSIIGAT QIKNTNKKAD FHGDHGAEKS SFKVRYPTVD YNLVRDLKGD   650
EATVRDTHSK RDTKCQSQSS AGEEKIAPTL RGGEIPDRKR PESVYSTSKD   700
TKYQSVYVLS AEKDECVIAT EV                                 722
```

FIG. 8

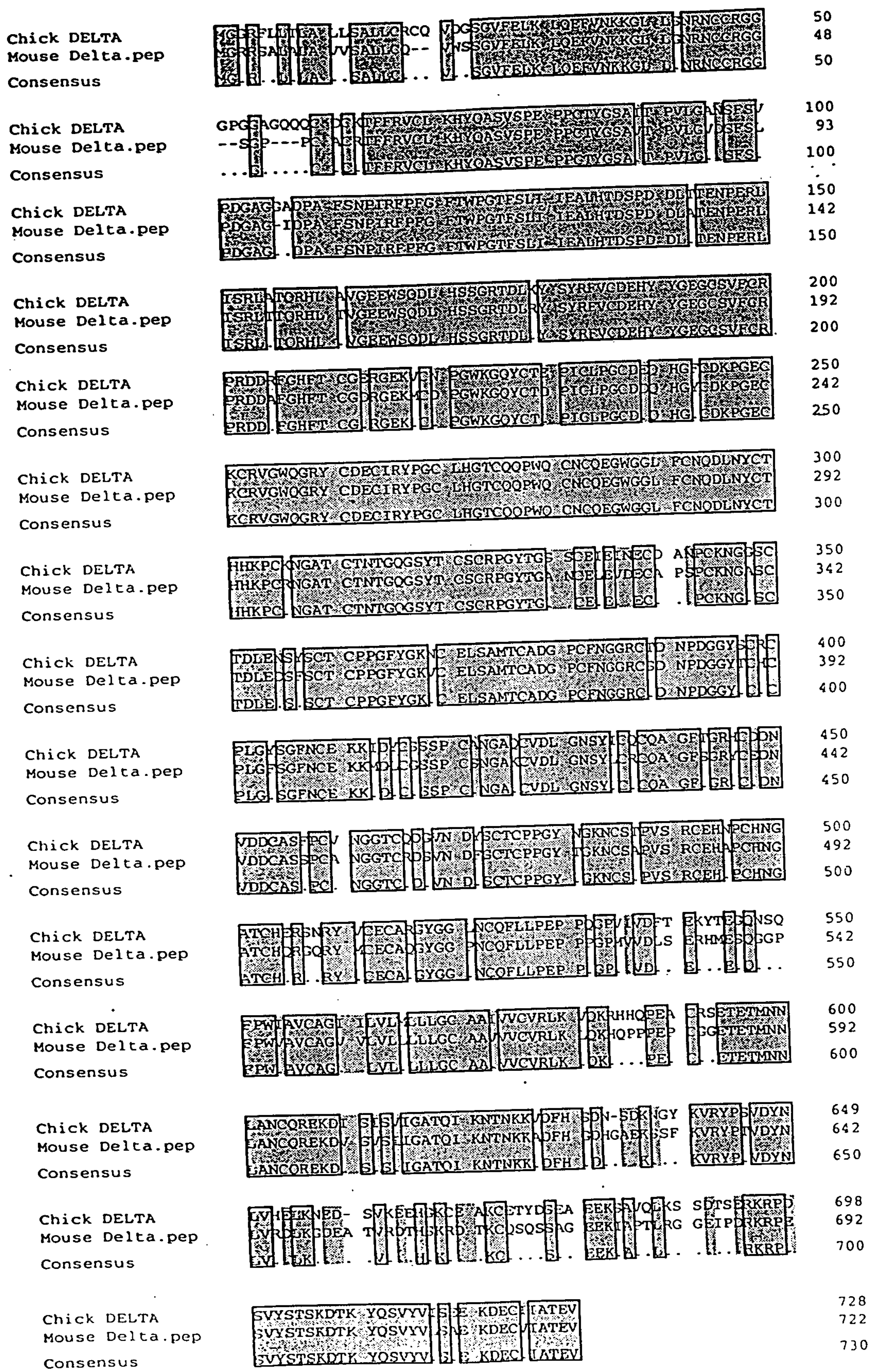

FIG. 9

```
        10         20         30         40         50         60
                    *                     *                     *
TACGATGAAY AACCTGGCGA ACTGCCAGCG TGAGAAGGAC ATCTCAGTCA GCATCATCGG
 Y  D  E  X  P  G  E  L  P  A  *  E  G  H  L  S  Q  H  H  R>
  T  M  N  N  L  A  N  C  Q  R  E  K  D  I  S  V  S  I  I  G>
   R  *  X  T  W  R  T  A  S  V  R  R  T  S  Q  S  A  S  S>

        70         80         90        100        110        120
                    *                     *                     *
GGCYACGTCA GATCARGAAC ACCAACAAGA AGGCGGACTT YMCASCGGGG GACCASAGCG
 G  X  V  R  S  X  T  P  T  R  R  R  T  X  X  R  G  T  X  A>
  A  T  S  D  Q  E  H  Q  Q  E  G  G  L  X  X  G  G  P  X  R>
G  X  R  Q  I  X  N  T  N  K  K  A  D  F  X  X  G  D  X  S>

       130        140        150        160        170        180
                    *                     *                     *
TCCGACAAGA ATGGMTTTCA AGGCCCCGCTA CCCCAGCGTG GACTATAACT CGTGCAGGAC
 S  D  K  N  G  F  Q  G  P  L  P  Q  R  G  L  *  L  V  Q  D>
  P  T  R  M  X  F  K  A  R  Y  P  S  V  D  Y  N  S  C  R  T>
V  R  Q  E  W  X  S  R  P  A  T  P  A  W  T  I  T  R  A  G>

       190        200        210        220        230        240
                    *                     *                     *
CTCAAGGGTG ACGACACCGC CGTCAGGACG TCGCACAGCA AGCGTGACAC CAAGTGCCAG
 L  K  G  D  D  T  A  V  R  T  S  H  S  K  R  D  T  K  C  Q>
  S  R  V  T  T  P  P  S  G  R  R  T  A  S  V  T  P  S  A  S>
P  Q  G  *  R  H  R  R  Q  D  V  A  Q  Q  A  *  H  Q  V  P>

       250        260        270        280        290        300
                    *                     *                     *
TCCCCAGGCT CCTCAGGGAG GAGAAGGGGA CCCCGACCAC ACTCAGGGGK TGCGTGCTGC
 S  P  G  S  S  G  R  R  R  G  P  R  P  H  S  G  X  A  C  C>
  P  Q  A  P  Q  G  G  E  G  D  P  D  H  T  Q  G  X  R  A  A>
V  P  R  L  L  R  E  E  K  G  T  P  T  T  L  R  G  C  V  L>

       310        320        330        340        350        360
                    *                     *                     *
GGGCCGGGCT CAGGAGGGGG TACCTGGGGG GTGTCTTCCT GGAACCACTG CTCCGTTTCT
 G  P  G  S  G  G  G  T  W  G  V  S  S  W  N  H  C  S  V  S>
  G  R  A  Q  E  G  V  P  G  G  C  L  P  G  T  T  A  P  F  L>
R  A  G  L  R  R  G  Y  L  G  G  V  F  L  E  P  L  L  R  F>
```

FIG. 10

```
        370          380          390          400          410          420
                      *                         *                         *
CTTCCCAAAT GTTCTCATGC ATTCATTGTG GATTTTCTCT ATTTTCCTTT TAGTGGAGAA
 L  P  K  C  S  H  A  F  I  V  D  F  L  Y  F  P  F  S  G  E>
  F  P  N  V  L  M  H  S  L  W  I  F  S  I  F  L  L  V  E  K>
S  S  Q  M  F  S  C  I  H  C  G  F  S  L  F  S  F  *  W  R>

        430          440          450          460          470          480
                      *                         *                         *
GCATCTGAAA GAAAAAGGCC GGACTCGGGC TGTTCAACTT CAAAAGACAC CAAGTACCAG
 A  S  E  R  K  R  P  D  S  G  C  S  T  S  K  D  T  K  Y  Q>
  H  L  K  E  K  G  R  T  R  A  V  Q  L  Q  K  T  P  S  T  S>
S  I  *  K  K  K  A  G  L  G  L  F  N  F  K  R  H  Q  V  P>

        490          500          510          520
                      *                         *
TCGGTGTACG TCATATCCGA GGAGAAGGAC GAGTGCGTCA TCGCA
 S  V  Y  V  I  S  E  E  K  D  E  C  V  I  A>
  R  C  T  S  Y  P  R  R  R  T  S  A  S  S>
V  G  V  R  H  I  R  G  E  G  R  V  R  H  R>
```

FIG. 10 (cont'd)

```
              .         .         .         .         .
  1 TMNNLANCQREKDISVSIIGATQIXNTNKKADFXXGDXSSDKNGFQKARY 50
    |||||||||||||||:|:|||||| |||||.||  ::  |||||: |.||
597 TMNNLANCQREKDISISVIGATQIKNTNKKVDFHSDN..SDKNGY.KVRY 643
              .         .         .         .         .
 51 PSVDYNLVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACC 100
    ||||||||::||.:| .|:..|:| :.||:. :|.:  :::
644 PSVDYNLVHELKNED.SVKEEHGKCEAKCETYDSEAEEKSA......... 683
              .         .         .         .         .
101 GPGSGGGTWGVSSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSG 150
                                 |::    |::.||||||||.
684 .............................VQLK....SSDTSERKRPDSV 700
              .         .
151 CSTSKDTKYQSVYVISEEKDECVIA 175
    :|||||||||||||||||||||:||
701 YSTSKDTKYQSVYVISEEKDECIIA 725
```

FIG. 11

```
        10         20         30         40         50         60
         *          *          *          *          *          *
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG

        70         80         90        100        110        120
         *          *          *          *          *          *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA

       130        140        150        160        170        180
         *          *          *          *          *          *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT

       190        200        210        220        230        240
         *          *          *          *          *          *
GACGGTGGGC CAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA

       250        260        270        280        290        300
         *          *          *          *          *          *
CTCCTACCGC TTCGTGTGTC ACCAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTCCCG

       310        320        330        340        350        360
         *          *          *          *          *          *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA

       370        380        390        400        410        420
         *          *          *          *          *          *
CCCTGGCTCG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA

       430        440        450        460        470        480
         *          *          *          *          *          *
GCATGGATTT TGTGACAAAC CACGGGAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA

       490        500        510        520        530        540
         *          *          *          *          *          *
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA

       550        560        570        580        590        600
         *          *          *          *          *          *
GTGCAACTGC CAGGAAGGNT GGGGGGCCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC

       610        620        630        640        650        660
         *          *          *          *          *          *
ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC

       670        680        690        700        710        720
         *          *          *          *          *          *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA

       730        740        750        760        770        780
         *          *          *          *          *          *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC

       790        800        810        820        830        840
         *          *          *          *          *          *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG

       850        860        870        880        890        900
         *          *          *          *          *          *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
```

FIG. 12A

```
        910        920        930        940        950        960
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC

        970        980        990       1000       1010       1020
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG

       1030       1040       1050       1060       1070       1080
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC

       1090       1100       1110       1120       1130       1140
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC

       1150       1160       1170       1180       1190       1200
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCACGTG CGAGCACGCA

       1210       1220       1230       1240       1250       1260
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGTGTGCC

       1270       1280       1290       1300       1310       1320
CGAAGCTACG GGGGTCCCAA CTCCCANTTC CTGCTCCCCG AAACTGCCCC CCCGGCCCCA

       1330       1340       1350       1360       1370       1380
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT

       1390       1400       1410       1420       1430       1440
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTC CTGGGCTGTG CCGCTGTGGT

       1450       1460       1470       1480       1490       1500
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA

       1510       1520       1530       1540       1550       1560
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT

       1570       1580       1590       1600       1610       1620
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG

       1630       1640       1650       1660       1670       1680
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA

       1690       1700       1710       1720       1730       1740
CCTCAAGGGT GACGACACCG CCGTCAGGCA CGCGCACAGC AAGCGTGACA CCAAGTGNCA

       1750       1760       1770       1780       1790       1800
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG

       1810       1820       1830       1840       1850       1860
```

FIG. 12A (cont'd)

AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA

1870 1880 1890 1900 1910 1920

NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG

1930 1940 1950 1960 1970 1980

AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCG GATTCCGNTT TCAAAGTTTT

T

FIG. 12A (cont'd)

```
        10         20         30         40         50         60      a.a. no.
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG
 H  W  V  R  A  P  L  E  V  D  G  I  D  K  L  D  I  E  F  R>   20
 I  G  Y  G  P  P  S  R  S  T  V  S  I  S  L  I  S  N  S  [G>] 20
 L  G  T  G  P  P  R  G  R  R  Y  R  *  A  *  Y  R  I  P>      19

        70         80         90        100        110        120
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA
 L  H  L  A  G  H  L  L  S  D  Y  *  S  S  P  H  R  F  S  *>   40
[F  T  W  P  G  T  F  S  L  I  I  E  A  L  H  T  D  S  P  D>]  40
 A  S  P  G  R  A  P  S  L  *  L  L  K  L  S  T  Q  I  L  L>   39

       130        140        150        160        170        180
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT
 *  P  R  N  R  K  P  R  K  T  H  Q  P  P  G  H  P  E  A  P>   60
[D  L  A  T  E  N  P  E  R  L  I  S  R  L  A  T  Q  R  H  L>]  60
 M  T  S  Q  Q  K  T  Q  K  D  S  S  A  A  W  P  P  R  G  T>   59

       190        200        210        220        230        240
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA
 D  G  G  R  G  V  V  P  G  P  A  Q  Q  R  P  H  G  P  Q  V>   80
[T  V  G  E  E  W  S  Q  D  L  H  S  S  G  R  T  D  L  K  Y>]  80
 *  R  W  A  R  S  G  P  R  T  C  T  A  A  A  A  R  T  S  S>   79

       250        260        270        280        290        300
CTCCTACCGC TTCGTGTGTG ACGAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG
 L  L  P  L  R  V  *  R  T  L  L  R  R  G  L  L  R  F  L  P>  100
[S  Y  R  F  V  C  D  E  H  Y  Y  G  E  G  C  S  V  F  C  R>] 100
 T  P  T  A  S  C  V  T  N  T  T  T  E  R  A  A  P  F  S  A>   99

       310        320        330        340        350        360
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA
 S  P  G  R  C  L  R  P  L  H  L  W  G  A  W  G  E  S  V  Q>  120
[P  R  D  D  A  F  G  H  F  T  C  G  E  R  G  E  K  V  C  N>] 120
 V  P  G  T  M  P  S  A  T  S  P  V  C  S  V  G  R  K  C  A>  119

       370        380        390        400        410        420
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA
 P  W  L  E  R  A  L  L  H  R  A  D  L  P  A  W  M  *  *  A>  140
[P  G  W  K  G  P  Y  C  T  E  P  I  C  L  P  G  C  D  E  Q>] 140
 T  L  A  G  K  G  P  T  A  Q  S  R  S  A  C  L  D  V  M  S>  139

       430        440        450        460        470        480
GCATGGATTT TGTGACAAAC CAGCCCAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA
 A  W  I  L  *  Q  T  R  G  M  Q  V  Q  S  G  L  A  G  P  V>  160
[H  G  F  C  D  K  P  G  E  C  K  C  R  V  G  W  Q  G  R  Y>] 160
 S  M  D  F  V  T  N  Q  G  N  A  S  A  E  W  A  G  R  A  G>  159

       490        500        510        520        530        540
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA
 L  *  R  V  Y  P  L  S  R  L  S  P  W  H  L  P  A  A  L  A>  180
```

FIG. 12B

```
 C  D  E  C  I  R  Y  P  G  C  L  H  G  T  C  Q  Q  P  W  Q>  180
T  V  T  S  V  S  A  I  Q  A  V  S  M  A  P  A  S  S  P  G>  179

      550       560       570       580       590       600
       *    *    *    *    *    *    *    *    *    *    *    *
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC
 V  Q  L  P  G  R  X  G  G  P  F  L  Q  P  G  P  E  L  L  H>  200
 C  N  C  Q  E  G  W  G  G  L  F  C  N  Q  D  L  N  Y  C  T>  200
S  A  T  A  R  K  X  G  G  A  F  S  A  T  R  T  *  T  T  A>  199

      610       620       630       640       650       660
       *    *    *    *    *    *    *    *    *    *    *    *
ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGCCCAG GGGGAGCTAC
 T  P  *  A  L  Q  E  W  S  H  L  Q  Q  T  R  A  R  G  S  Y>  220
 H  H  K  P  C  K  N  G  A  T  C  N  K  H  G  P  G  G  A  T>  220
H  T  I  S  P  A  R  M  E  P  P  A  T  N  T  G  Q  G  E  L>  219

      670       680       690       700       710       720
       *    *    *    *    *    *    *    *    *    *    *    *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA
 T  W  S  L  A  G  L  G  Y  X  G  C  H  L  R  S  L  G  I  G>  240
 L  G  L  W  P  X  W  G  T  X  G  A  T  C  E  A  W  G  L  D>  240
H  L  V  F  G  R  X  G  V  X  R  V  P  P  A  K  L  G  D  W>  239

      730       740       750       760       770       780
       *    *    *    *    *    *    *    *    *    *    *    *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC
 R  V  V  D  P  S  P  W  *  E  R  R  E  L  D  G  S  S  E  N>  260
 E  L  L  T  P  A  L  G  K  N  G  G  S  L  T  D  L  R  R  T>  260
T  S  C  *  P  Q  P  L  V  R  T  E  G  A  *  R  I  F  G  E>  259

      790       800       810       820       830       840
       *    *    *    *    *    *    *    *    *    *    *    *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG
 S  Y  S  C  T  C  P  P  G  F  Y  G  K  I  C  E  L  S  A  M>  280
 A  T  P  V  P  A  H  P  A  S  T  A  K  S  V  N  *  V  P  *>  280
Q  L  L  L  Y  L  P  T  R  L  L  R  Q  N  L  *  I  E  C  H>  279

      850       860       870       880       890       900
       *    *    *    *    *    *    *    *    *    *    *    *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
 T  C  A  D  G  P  C  F  N  G  G  R  C  S  D  S  P  D  G  G>  300
 P  V  R  T  A  L  A  L  T  G  V  G  A  Q  T  A  P  M  E  G>  300
D  L  C  G  R  P  L  L  *  R  G  S  V  L  R  Q  P  R  W  R>  299

      910       920       930       940       950       960
       *    *    *    *    *    *    *    *    *    *    *    *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC
 Y  S  C  R  C  P  V  G  Y  S  G  F  N  C  E  K  K  I  D  Y>  320
 T  A  A  A  A  P  W  A  T  P  A  S  T  V  R  R  K  L  T  T>  320
V  Q  L  P  L  P  R  G  L  L  R  L  Q  L  *  E  E  N  *  L>  319

      970       980       990      1000      1010      1020
       *    *    *    *    *    *    *    *    *    *    *    *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG
 C  S  S  S  P  C  S  N  G  A  K  C  V  D  L  G  D  A  Y  L>  340
 A  A  L  H  P  V  L  M  V  P  S  V  W  T  S  V  M  P  T  C>  340
L  Q  L  F  T  L  F  *  W  C  Q  V  C  G  P  R  *  C  L  P>  339

     1030      1040      1050      1060      1070      1080
       *    *    *    *    *    *    *    *    *    *    *    *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC
```

FIG. 12B (cont'd)

```
C R C  Q A G F  S G R  H C D  D N V D  D C A>  360
 A A A  R P A  S R G G  T V T  T T W  T T A P>  360
V P L P  G R L  L G F  A L * R  Q R G  R L R>  359

     1090       1100       1110       1120       1130       1140
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC
 S S P  C A N G  G T C  R D G  V N D F  S C T>  380
 P P R  A P T  G A P A  G M A  * T T  S P A P>  380
L L P V  R Q R  G H L  P G W R  E R L  L L H>  379

     1150       1160       1170       1180       1190       1200
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCAGGTG CGAGCACGCA
 C P P  G Y T G  R N C  S A P  A S R C  E H A>  400
 A R L  A T R  A G T A  V P P  P A G  A S T H>  400
L P A W  L H G  Q E L  Q C P R  Q Q V  R A R>  399

     1210       1220       1230       1240       1250       1260
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGTGTGCC
 P C H  N G A T  C H E  R G H  R Y X  C E C A>  420
 P A T  M G P  P A T R  G A T  A I C  A S V P>  420
T L P Q  W G H  L P R  E G P P  L F V  R V C>  419

     1270       1280       1290       1300       1310       1320
CGAAGCTACG GGGGTCCCAA CTGCCANTTC CTGCTCCCCG AAACTGCCCC CCCGGCCCCA
 R S Y  G G P N  C X F  L L P  E T A P  P A P>  440
 E A T  G V P  T A X S  C S P  K L P  P R P H>  440
P K L R  G S Q  L P X  P A P R  N C P  P G P>  439

     1330       1340       1350       1360       1370       1380
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT
 R W W  K L P *  K N L  K G P  G G A H  P L G>  460
 G G G  N S P  K K T *  K G R  G G P  I P L V>  460
T V V F  T P L  K K P  K R A G  G G P  S P W>  459

     1390       1400       1410       1420       1430       1440
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTC CCGCTGTGGT
 G R V  R R G H  P C P  H A A  A G L C  R C G>  480
- D V C  A G V  I L V L  M L L  L G C  A A V V>  480
W T C A  P G S  S L S  S C C C  W A V  P L W>  479

     1450       1460       1470       1480       1490       1500
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA
 G L R  P A E A  A E A  P A P  S R P L  X G G>  500
 V C V  R L R  L Q K H  R P P  A D P  X R G E>  500
W S A S  G * G  C R S  T G P Q  P T P  X G G>  499

     1510       1520       1530       1540       1550       1560
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT
 D G D  H E Q P  G Q L  P A *  E G H L  S Q H>  520
 T E T  M N N L  X N C  Q R E  K D I S  V S I>  520
R R R P  * T T  W X T  A S V R  R T S  Q S A>  519

     1570       1580       1590       1600       1610       1620
```

FIG. 12B (cont'd)

```
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG
 H  R  G   H  A  D  Q   E  H  Q   Q  E  G   G  L  P  R   G  P  Q>  540
 I  G  X   T  Q  I  K   N  T  N   K  K  A   D  F  H  G   D  H  X>  540
S  S  G  X  R  R  S   R  T  P   T  R  R  R   T  S  T   Q  T  T>   539

        1630      1640      1650      1660      1670      1680
          *    *    *    *    *    *    *    *    *    *    *    *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCACNGGTG GACTATAACC TCGTGCAGGA
 X  R  Q   E  W  L  Q   G  P  L   P  X  G   G  L  *  P   R  A  G>  560
 A  D  K   N  G  F   K  A  R  Y   P  X  V   D  Y  N   L  V  Q  D>  560
X  P  T  R   M  A  S   R  P  A  T  Q  X  W   T  I  T   S  C  R>   559

        1690      1700      1710      1720      1730      1740
          *    *    *    *    *    *    *    *    *    *    *    *
CCTCAAGGGT GACGACACCG CCGTCAGGGA CGCGCACAGC AAGCGTGACA CCAAGTGNCA
 P  Q  G   *  R  H  R   R  Q  G   R  A  Q   Q  A  *  H   Q  V  X>  580
 L  K  G   D  D  T   A  V  R  D   A  H  S   K  R  D   T  K  X  Q>  580
T  S  R  V   T  T  P   P  S  G   T  R  T  A   S  V  T   P  S  X>   579

        1750      1760      1770      1780      1790      1800
          *    *    *    *    *    *    *    *    *    *    *    *
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG
 A  P  G   L  L  R  G   G  K  G   D  P  R   P  T  L  R   G  W  R>  600
 P  Q  G   S  S  G   E  E  K  G   T  P  D   P  H  S   G  G  G  G>  600
S  P  R  A   P  Q  G   R  R  R   C  P  P  T   H  T  Q   G  V  R>   599

        1810      1820      1830      1840      1850      1860
          *    *    *    *    *    *    *    *    *    *    *    *
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA
 K  H  L   E  R  K  R   P  D  F   G  L  V   Q  L  S  K   D  X  Q>  620
 S  I  L   K  E  K   G  R  T  S   G  L  F   N  F  Q   K  T  X  X>  620
E  A  S  *   K  K  K   A  G  L   R  A  C  S   T  F  K   R  Q  X>   619

        1870      1880      1890      1900      1910      1920
          *    *    *    *    *    *    *    *    *    *    *    *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG
 X  T  S   R  C  X  S   F  P  X   E  E  G   *  L  R  H   R  X  L>  640
 V  Q  V   G  V  R   H  F  R  R   R  K  X   D  C  V   I  G  X  *>  640
X  Y  K  S   V  X  V   I  S  X   G  G  R  X   T  A  S   *  E  X>   639

        1930      1940      1950      1960      1970      1980
          *    *    *    *    *    *    *    *    *    *    *    *
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCG GATTCCCNTT TCAAAGTTTT
 R  X  *   X  G  S  *   X  W  K   X  X  P   G  F  R  F   Q  S  F>  660
 G  X  K   X  X  V   X  X  G  K   X  S  P   D  S  X   F  K  V  F>  660
E  V  V  X   W  X  L   X  L  E   X  X  P  R   I  P  X   S  K  F>   659

T
```

FIG. 12B (cont'd)

Mouse Delta vs Partial Human Delta

Mouse Delta DNA	GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT	50
Human Delta	---------- ---------- ---------- ---------- ----------	
Consensus	GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT	50
Mouse Delta DNA	CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG	100
Human Delta	---------- ---------- ---------- ---------- ----------	
Consensus	CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG	100
Mouse Delta DNA	CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG	150
Human Delta	---------- ---------- ---------- ---------- ----------	
Consensus	CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG	150
Mouse Delta DNA	CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC	200
Human Delta	---------- ---------- ---------- ---------- ----------	
Consensus	CGGGGGCTCT GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC	200
Mouse Delta DNA	TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC	250
Human Delta	---------- ---------- ---------- ---------- ----------	
Consensus	TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC	250
Mouse Delta DNA	AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTGATGG	300
Human Delta	---------- ---------- ---------- ---------- -----CATGG	5
Consensus	AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTSATGG	300
Mouse Delta DNA	CGGAGGCATC GACCGC---G GCTTCGGCAA CCCCA--TCC GATGTC-CCC	343
Human Delta	GGTAGGGGCC CCCCTCGAGG TCGACGGTAT CGATAAGCTT GATATCGAAT	55
Consensus	SGMARGSRYC SMCCMCGAGG MCKWCRGMAW CSMYAAGYYY GATNTCGMMY	350
Mouse Delta DNA	TTCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATCATTG AAGCCCTCCA	393
Human Delta	TTCGGCTTCA CCTGGCCTGG CACCTTCTCT CTGATTATTG AAGCTCTCCA	105
Consensus	TYCGGCTTCA CCTGGCCRGG MACCTTCTCT CTGATMATTG AAGCMCTCCA	400
Mouse Delta DNA	TACAGACTCT CCCGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA	443
Human Delta	CACAGATTCT CCTGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA	155
Consensus	YACAGAYTCT CCYGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA	450
Mouse Delta DNA	GCCGCCTGAC CACACAGAGG CACCTCACTG TGGGAGAAGA ATGGTCTCAG	493
Human Delta	GCCGCCTGGC CACCCAGAGG CACCTGACGG TGGGCGAGGA GTGGTCCCAG	205
Consensus	GCCGCCTGRC CACMCAGAGG CACCTSACKG TGGGMGARGA RTGGTCMCAG	500
Mouse Delta DNA	GACCTTCACA GTAGCGGCCG CACAGACCTC CGGTACTCTT ACCGTTTTGT	543
Human Delta	GACCTGCACA GCAGCGGCCG CACGGACCTC AAGTACTCCT ACCGCTTCGT	255
Consensus	GACCTKCACA GYAGCGGCCG CACRGACCTC MRGTACTCYT ACCGYTTYGT	550
Mouse Delta DNA	GTGTGACGAG CACTACTACG GAGAAGGTTG CTCTGTTTTC TGCCGACCTC	593
Human Delta	GTGTGACCAA CACTACTACG GAGAGGGCTG CTCCGTCTTC TGCCGTCCCC	305
Consensus	GTGTGACSAR CACTACTACG GAGARGGYTG CTCYGTYTTC TGCCGWCCYC	600
Mouse Delta DNA	GGGATGACGC CTTTGGCCAC TTCACCTGCG GGGACAGAGG GGAGAAGATG	643
Human Delta	GGGACGATGC CTTCGGCCAC TTCACCTGTG GGGAGCGTGG GGAGAAAGTG	355
Consensus	GGGAYGAYGC CTTYGGCCAC TTCACCTGYG GGGASMGWGG GGAGAARRTG	650

FIG. 13

Mouse Delta vs Partial Human Delta

```
Mouse Delta DNA   TGCGACCCTG GCTGGAAAGG GCAGTACTGC ACTGAGCCAA TCTGTCTGCC    693
Human Delta       TGCAACCCTC CCTGGAAAGG ACCCTACTGC ACAGACCCGA TCTGCCTGCC    405
Consensus         TGCRACCCTG GCTGGAAAGG RCMSTACTGC ACWGASCCRA TCTGMCTGCC    700

Mouse Delta DNA   AGGGTGTGAT GATCAACATG GATACTGTGA CAAACCAGGG GAGTGCAAGT    743
Human Delta       TGGATCTCAT GAGCAGCATG GATTTTGTGA CAAACCAGGG GAATGCAAGT    455
Consensus         WGGRTGTGAT GASCARCATG GATWYTGTGA CAAACCAGGG GARTGCAAGT    750

Mouse Delta DNA   GCAGAGTTGG CTGGCAGGGC CGTTACTGCG ATGAGTGTAT CCGATACCCA    793
Human Delta       GCAGAGTGGG CTGGCAGGGC CCTTACTGTG ACGAGTGCAT CCGCTATCCA    505
Consensus         GCAGAGTKGG CTGGCAGGGC CSTTACTGYG AYGAGTGYAT CCGMTAYCCA    800

Mouse Delta DNA   GGTTGTCTCC ATGGCACCTG CCAGCAACCC TGGCAGTGTA ACTGCCAGGA    843
Human Delta       GGCTGTCTCC ATGGCACCTG CCAGCAGCCC TGGCAGTGCA ACTGCCAGGA    555
Consensus         GGYTGTCTCC ATGGCACCTG CCAGCARCCC TGGCAGTGYA ACTGCCAGGA    850

Mouse Delta DNA   AGGCTGGGGG GGCCTTTTCT GCAACCAAGA CCTGAACTAC TGTACTCACC    893
Human Delta       AGGTTGGGGG GGCCTTTTCT GCAACCAGGA CCTGAACTAC TGCACACACC    605
Consensus         AGGYTGGGGG GGCCTTTTCT GCAACCARGA CCTGAACTAC TGYACWCACC    900

Mouse Delta DNA   ATAAGCCCTG CAGGAATGGA GCCACCTGCA -CCAACACGG GCCAGGGG-A    941
Human Delta       ATAAGCCTTG CAAGAATGGA GCCACCTGCA ACAAACACGG GCCAGGGGGA    655
Consensus         ATAAGCCYTG CARGAATGGA GCCACCTGCA ACMAACACGG GCCAGGGGGA    950

Mouse Delta DNA   GCTACACATG TTCTT--GCC -GACCTGGGT ATACA-GGTG CCAACTGTG-    986
Human Delta       GCTACACTTG GTCTTTGGCC GGNCTGGGGT ACANAGGGTG CCAGCTGCGA    705
Consensus         GCTACACWTG KTCTTTGGCC GGNCYKGGGT AYANAGGGTG CCARCTGYGA   1000

Mouse Delta DNA   AGCT--GGAA GTAGATGAG- TG-TGCTCCT AGCCCCT-GC AAGAACGGAG   1031
Human Delta       AGCTTGGGGA TTGGACGAGT TGTTGACCCC AGCCCTTGGT AAGAACGGAG    755
Consensus         AGCTTGGGRA KTRGAMGAGT TGTTGMYCCY AGCCCYTGGY AAGAACGGAG   1050

Mouse Delta DNA   CGAGCTGCAC GGACCTT--G AGCACAGCTT CTCTTGCACC TGCCCTCCCG   1079
Human Delta       GGAGCTTCAC GGATCTTCGG AGAACAGCTA CTCCTGTACC TGCCCACCCG    805
Consensus         SGAGCTKSAC GGAYCTTCGG AGRACAGCTW CTCYTGYACC TGCCCWCCCG   1100

Mouse Delta DNA   GCTTCTATGG CAAGGTCTGT GAGCTGACTC CCATGACCTG TGCAGATGGC   1129
Human Delta       GCTTCTACGG CAAAATCTGT GAATTGAGTG CCATGACCTG TGCGGACGGC    855
Consensus         GCTTCTAYGG CAARRTCTGT GARYTGAGMG CCATGACCTG TGCRGAYGGC   1150

Mouse Delta DNA   CCTTGCTTCA ATGGAGGACG ATGTTCAGAT ACCCCTGACG GAGGCTACAC   1179
Human Delta       CCTTGCTTTA ACGGCGGTCG GTGCTCAGAC AGCCCCGATG GAGGGTACAG    905
Consensus         CCTTGCTTYA AYGGRGGWCG RTGYTCAGAY ARCCCYGAYG GAGGSTACAS   1200

Mouse Delta DNA   CTGCCATTGC CCCTTGGGCT TCTCTGGCTT CAACTGTGAG AAGAAGATGG   1229
Human Delta       CTGCCGCTGC CCCGTGCCCT ACTCCGGCTT CAACTGTGAG AAGAAAATTG    955
Consensus         CTGCCRYTGC CCCKTGGGCT WCTCYGGCTT CAACTGTGAG AAGAARATKG   1250

Mouse Delta DNA   ATCTCTGCGG CTCTTCTCCT TGTTCTAACG GTGCCAAGTG TGTGGACCTC   1279
Human Delta       ACTACTGCAG CTCTTCACCC TGTTCTAATG GTGCCAAGTG TGTGGACCTC   1005
Consensus         AYYWCTGCRG CTCTTCMCCY TGTTCTAAYG GTGCCAAGTG TGTGGACCTC   1300
```

FIG. 13 (cont'd)

Mouse Delta vs Partial Human Delta

```
Mouse Delta DNA   GGCAACTCTT ACCTGTGCCG TTCCCAGGCT GGCTTCTCTG GGAGGTACTG   1329
Human Delta       GGTGATGCCT ACCTGTGCCG TTGCCAGGCC GGCTTCTCGG GGAGGCACTG   1055
Consensus         GGYRAYNCYT ACCTGTGCCG KTGCCAGGCY GGCTTCTCKG GGAGGYACTG   1350

Mouse Delta DNA   CGAGGACAAT GTGGATGACT GTGCCTCCTC CCCGTGTGCA AATGGGGGCA   1379
Human Delta       TGATGACAAC GTGGACGACT GCGCCTCCTC CCCGTGCGCC AACGGGGGCA   1105
Consensus         YGASGACAAY GTGGAYGACT GYGCCTCCTC CCCGTGYGCM AAYGGGGGCA   1400

Mouse Delta DNA   CCTGCCGGGA CAGTGTGAAC GACTTCTCCT GTACCTGCCC ACCTGGCTAC   1429
Human Delta       CCTGCCGGGA TGGCGTGAAC GACTTCTCCT GCACCTGCCC GCCTGGCTAC   1155
Consensus         CCTGCCGGGA YRGYGTGAAC GACTTCTCCT GYACCTGCCC RCCTGGCTAC   1450

Mouse Delta DNA   ACGGGCAAGA ACTGCAGTGC CCCTGTCAGC AGGTGTGAGC ATGCACCCTG   1479
Human Delta       ACGGGCACGA ACTGCAGCGC CCCCGGCAGC AGGTGCGAGC ACGCACCCTG   1205
Consensus         ACGGGCAMGA ACTGCAGYGC CCCYGKCAGC AGGTGYGAGC AYGCACCCTG   1500

Mouse Delta DNA   CCATAATGGG GCCACCTGCC ACCAGAGGGG CCAGCGCTAC ATGTGTGAGT   1529
Human Delta       CCACAATGGG GCCACCTGCC ACGAGAGGGG CCACCGCTAT TTGTGCGAGT   1255
Consensus         CCAYAATGGG GCCACCTGCC ACSAGAGGGG CCASCGCTAY WTGTGYGAGT   1550

Mouse Delta DNA   GCGCCCAGGG CTATGGCGGC CCCAACTGCC AGTTTCTGCT CCCTG-AGCC   1578
Human Delta       GTGCCCGAAG CTACGGGGGT CCCAACTGCC ANTTCCTGCT CCCCGAAACT   1305
Consensus         GYGCCCRRRG CTAYGGSGGY CCCAACTGCC ANTTYCTGCT CCCYGMARCY   1600

Mouse Delta DNA   -ACCACCAGG TCCCATGGTG GTGG-ATCTC AGTGATAGGC ATAT-GCAGA   1625
Human Delta       GCCCCCCCGG CCCCACGGTG GTGGAAACTC CCCTAAAAAA ACCTAAAAGG   1355
Consensus         GMCCMCCMGG YCCCAMGGTG GTGGAAMCTC MSYHARARRM AYMTARRAGR   1650

Mouse Delta DNA   GCCAGGGTGG GCCCTTCCCC TGCCTCCTCC TGTGTGCCGG GGTGGTGCTT   1675
Human Delta       GCCGGGGGGG GCCCATCCCC TTCCTCGACG TGTGCGCCGG GGTCATCCTT   1405
Consensus         GCCRGGGSGG GCCCWTCCCC TKSCTCSMCG TGTGYGCCGG GGTSRTSCTT   1700

Mouse Delta DNA   GTCCTCTTGC TGCTGCTGGG CTGTGCTGCT GTGGTGGTCT GCGTCCGGCT   1725
Human Delta       GTCCTCATGC TGCTGCTGGG CTGTGCCGCT GTGGTGGTCT GCGTCCGGCT   1455
Consensus         GTCCTCWTGC TGCTGCTGGG CTGTGCYGCT GTGGTGGTCT GCGTCCGGCT   1750

Mouse Delta DNA   GAAGCTACAG AAACACCAGC CTCCACTTGA ACCCTGTGGG GGAGAGACAG   1775
Human Delta       GAGGCTGCAG AAGCACCGGC CCCCACCTGA CCCCTGNCGG GGGGAGACGG   1505
Consensus         GARGCTRCAG AARCACCRGC CYCCAYYTGA MCCCTGNSGG GGRGAGACRG   1800

Mouse Delta DNA   AAACCATGAA CAACCTAGGC AATTGCCAGC CGGACAAGGA CTTTTCTGTT   1825
Human Delta       AGACCATGAA CAACCTGGAC AACTCCCACC GTGAGAAGGA CATCTCAGTC   1555
Consensus         ARACCATGAA CAACCTRGMC AAYTSCCASC SKGASAAGGA CWTYTCWGTY   1850

Mouse Delta DNA   AGCATCATTG GGGCTACTCA GATCAAGAAC ACCAACAAGA AGGCGGACTT   1875
Human Delta       AGCATCATCG GGGNCACGCA GATCAAGAAC ACCAACAAGA AGGCGGACTT   1605
Consensus         AGCATCATYG GGGNYACKCA GATCAAGAAC ACCAACAAGA AGGCGGACTT   1900

Mouse Delta DNA   TCACGCCGAC CATGGAGCCA AGAAGAGCAG CTTTAAGGTC CGATACCCCA   1925
Human Delta       CCACCCCCAC CACAGNGCCG ACAAGAATGG CTTCAAGGCC CGCTACCCAG   1655
Consensus         YCACGCGGAC CAYRGNGCCR ASAAGARYRG CTTYAAGGYC CGMTACCCMR   1950
```

FIG. 13 (cont'd)

Mouse Delta vs Partial Human Delta

Mouse Delta DNA	CTGTGGACTA TAACCTCGTT CGAGACCTCA AGGGAGATGA AGCCACGGTC	1975
Human Delta	NGGTGGACTA TAACCTCGTG CAGGACCTCA AGGGTGATGA CACCTCCGTC	1705
Consensus	NKGTGGACTA TAACCTCGTK CRRGACCTCA AGGGWGAKGA MRCCRCSGTC	2000
Mouse Delta DNA	AGGGATACAC ACAGCAAACG TGACACCAAG TGCCAGTCAC AGAGCTCTGC	2025
Human Delta	AGGGACCGCC ACAGCAAGCG TCACACCAAG TGNCAGCCCC AGGGCTCCTC	1755
Consensus	AGGGAYRCRC ACAGCAARCG TGACACCAAG TGNCAGYCMC AGRGCTCYKC	2050
Mouse Delta DNA	AGGAGAAGAG AA---GATCG CC--CCAACA CTTA-GGGGT GG-GG-AGAT	2067
Human Delta	ACGGGAGGAG AAGGGGAGCC CCGACCGACA CTCAGGGGGT GGAGGAAGCA	1805
Consensus	AGGRGARGAG AAGGGGAKCS CCGACCMACA CTMAGGGGGT GGAGGAAGMW	2100
Mouse Delta DNA	TCCTGACAGA AAAAGGCCAG AGTCT--GTC TACTCTAC-T TCAAAGGAC-	2113
Human Delta	TCTTGAAAGA AAAAGGCCGG ACTTCGGGCT TGTTCAACTT TCAAAAGACA	1855
Consensus	TCYTGAMAGA AAAAGGCCRG ASTYYGGGYY TRYTCWACTT TCAAARGACA	2150
Mouse Delta DNA	-ACCAAGTAC CAGTCGGTGT ATGTTCTCTC TGCAGAA--A AGGATGAGTG	2160
Human Delta	ANCAANGTAC AAGTCGGTGT NCGTCATTTC CGNAGGAGGA AGGNTGACTG	1905
Consensus	ANCMANGTAC MAGTCGGTGT NYGTYMTKTC YGNAGRAGGA AGGNTGASTG	2200
Mouse Delta DNA	TGTTATA-GC GACTGAGCT- GTAAGATGGA AGCGATGTGG CAAAATTCCC	2208
Human Delta	CGTCATAGGA ANTTGAGGTN GTAAANTGGN AG---T-TG- --ANNTT---	1945
Consensus	YGTYATAGGM RNYTGAGCTN GTAARNTGGN AGCGATGTGG CAANNTTCCC	2250
Mouse Delta DNA	ATTTCTCTCA AATAAAATTC CAAGGATATA GCCCCGATGA ATGCTTCTGA	2258
Human Delta	-------GGA AAGNNN-TC CCCGGAT--- --TCCGNT-- ----TTC---	1972
Consensus	ATTTCTCKSA AAKNNNATYC CMMGGATATA GCYCCGNTGA ATGCTKCTGA	2300
Mouse Delta DNA	GAGACGAAGG GAGAGGAAAC CCACGGACTG CTGCTGAGAA CCAGGTTCAG	2308
Human Delta	---------- ------AAA- ---------G TTTTT----- ----------	1981
Consensus	GAGAGGAAGG GAGAGGAAAC CCAGGGACTG MTKYTGAGAA CCAGGTTCAG	2350
Mouse Delta DNA	GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT	2358
Human Delta	---------- ---------- ---------- ---------- ----------	1981
Consensus	GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT	2400
Mouse Delta DNA	AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG	2408
Human Delta	---------- ---------- ---------- ---------- ----------	1981
Consensus	AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG	2450
Mouse Delta DNA	GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA	2458
Human Delta	---------- ---------- ---------- ---------- ----------	1981
Consensus	GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA	2500
Mouse Delta DNA	TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA	2508
Human Delta	---------- ---------- ---------- ---------- ----------	1981
Consensus	TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA	2550
Mouse Delta DNA	GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC	2558
Human Delta	---------- ---------- ---------- ---------- ----------	1981
Consensus	GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC	2600

FIG. 13 (cont'd)

Mouse Delta vs Partial Human Delta

```
Mouse Delta DNA   TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT   2608
Human Delta       ---------- ---------- ---------- ---------- ----------   1981

Consensus         TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT   2650

Mouse Delta DNA   TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT   2658
Human Delta       ---------- ---------- ---------- ---------- ----------   1981

Consensus         TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT   2700

Mouse Delta DNA   ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA   2708
Human Delta       ---------- ---------- ---------- ---------- ----------   1981

Consensus         ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA   2750

Mouse Delta DNA   AAGGCACTTC GGGTCTATGT GACTATATTT TTTTGTATAT AAATGTATTT   2758
Human Delta       ---------- ---------- ---------- ---------- ----------   1981

Consensus         AAGGCACTTC GGGTCTATGT GACTATATTT TTTTGTATAT AAATGTATTT   2800

Mouse Delta DNA   ATGGAATATT GTGCAAATGT TATTTGAGTT TTTTACTGTT TTGTTAATGA   2808
Human Delta       ---------- ---------- ---------- ---------- ----------   1981

Consensus         ATGGAATATT GTGCAAATGT TATTTGAGTT TTTTACTGTT TTGTTAATGA   2850

Mouse Delta DNA   AGAAATTCAT TTTAAAAATA TTTTTCCAAA ATAAATATAA TGAACTACA    2857
Human Delta       ---------- ---------- ---------- ---------- ---------    1981

Consensus         AGAAATTCAT TTTAAAAATA TTTTTCCAAA ATAAATATAA TGAACTACA    2899
```

FIG. 13 (cont'd)

G F T W P G T F S L I I E A L H T D S P D> 21
D L A T E N P E R L I S R L A T Q R H L> 41
T V G E E W S Q D L H S S G R T D L K Y> 61
S Y R F V C D E H Y Y G E G C S V F C R> 81
P R D D A F G H F T C G E R G E K V C N> 101
P G W K G P Y C T E P I C L P G C D E Q> 121
H G F C D K P G E C K C R V G W Q G R Y> 141
C D E C I R Y P G C L H G T C Q Q P W Q> 161
C N C Q E G W G G L F C N Q D L N Y C T> 181
H H K P C K N G A T C * T N T G Q G * 198
S Y T * P S P * K N G G S L T D L * 213
E N S Y S C T C P P G F Y G K I C E L S A M> 235
T C A D G P C F N G G R C S D S P D G G> 255
Y S C R C P V G Y S G F N C E K K I D Y> 275
C S S S P C S N G A K C V D L G D A Y L> 295
C R C Q A G F S G R H C D D N V D D C A> 315
S S P C A N G G T C R D G V N D F S C T> 335
C P P G Y T G R N C S A P A S R C E H A> 355
P C H N G A T C H E R G H R Y * C E C A> 374
R S Y G G P N C * F L L P E * P P G P * 391
V V * L L L G C A A V V V C V R L R L Q K H> 412
R P P A D P * R G E T E T M N N L * 428
N C Q R E K D I S V S I I G * T Q I K N T N> 449
K K A D F H G D H * A D K N G F K A R Y P * 469
V D Y N L V Q D L K G D D T A V R D A H S K R D T K * 495
Q P Q G S S G E E K G T P * P T L R * G G * 514
T * R K R P * S * S T * S K D * T * 526
C V I * E V * 531

FIG. 14